

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:43:09 ; Search time 38.23 Seconds

(without alignments)
1128.209 Million cell updates/sec

Title: US-09-483-543a-9

Perfect score: 1733

Sequence: 1 KRGGAGNFDSEERSWTWGR.....SGCGXGLEVLFGQVRRKXG 326

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_vertebrate:*
15: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1078	62.2	239	11	Q9QW60	Q9QW60 mus sp. grb
2	834.5	48.2	255	14	Q99059	Q99059 avian sarco
3	343	19.8	279	5	Q9NHC3	Q9NHC3 caenorhabdi
4	213	12.3	217	13	Q9PU11	Q9PU11 xenopus lae
5	200	11.5	600	5	Q9VE96	Q9VE96 drosophila
6	193	11.1	1067	13	Q9YHU6	Q9YHU6 xenopus lae
7	184.5	10.6	1010	13	Q9YHU7	Q9YHU7 xenopus lae
8	182	10.5	1097	5	Q9U2T9	Q9U2T9 caenorhabdi
9	173	10.0	640	4	Q60593	Q60593 homo sapien
10	170	9.8	816	4	Q60592	Q60592 homo sapien
11	165	9.5	1270	13	Q42287	Q42287 xenopus lae
12	164	9.5	1196	11	Q35413	Q35413 rattus norv
13	163.5	9.4	857	3	Q9P7E8	Q9P7E8 schizosacch
14	163	9.4	884	4	Q9Y338	Q9Y338 homo sapien
15	162	9.3	815	4	Q9P200	Q9P200 homo sapien
16	162	9.3	1217	11	Q9WVE9	Q9WVE9 rattus norv
17	161	9.3	1094	5	Q61618	Q61618 drosophila
18	161	9.3	1097	5	Q9VIF7	Q9VIF7 drosophila

20	161	9.3	1100	4	Q94875	Q94875 homo sapien
21	160	9.2	1721	4	Q95216	Q95216 homo sapien
22	159	9.2	1220	4	Q9UE75	Q9UE75 homo sapien
23	159	9.2	1721	4	Q9UNK2	Q9UNK2 homo sapien
24	158	9.1	1004	4	Q9UHN7	Q9UHN7 homo sapien
25	158	9.1	1220	4	Q9UNK1	Q9UNK1 homo sapien
26	157.5	9.1	820	11	Q9QZK2	Q9QZK2 mus musculu
27	157	9.1	1248	4	Q9NZM2	Q9NZM2 homo sapien
28	157	9.1	1676	4	Q9ULG4	Q9ULG4 homo sapien
29	157	9.1	1681	4	Q9NYG0	Q9NYG0 homo sapien
30	157	9.1	1696	4	Q9NZM3	Q9NZM3 homo sapien
31	156.5	9.0	330	4	Q9NRR7	Q9NRR7 homo sapien
32	156.5	9.0	500	5	Q9V5J3	Q9V5J3 drosophila
33	156	9.0	939	5	Q24145	Q24145 drosophila
34	155	8.9	505	5	Q97337	Q97337 paracentrot
35	154.5	8.9	684	11	Q62417	Q62417 mus musculu
36	154.5	8.9	714	11	Q9Z0Z8	Q9Z0Z8 mus musculu
37	154.5	8.9	724	11	Q9Z0Z9	Q9Z0Z9 mus musculu
38	154	8.9	825	4	Q75815	Q75815 mus sapien
39	153	8.8	1714	11	Q9Z0R4	Q9Z0R4 mus sapien
40	152.5	8.8	1011	5	Q61639	Q61639 drosophila
41	152	8.8	954	5	Q97180	Q97180 drosophila
42	151.5	8.7	334	5	Q9PYT3	Q9PYT3 caenorhabdi
43	151	8.7	1146	11	Q9WVE1	Q9WVE1 rattus norv
44	151	8.7	1186	5	Q61080	Q61080 acanthamoeb
45	150.5	8.7	687	11	Q9QY53	Q9QY53 mus musculu

ALIGNMENTS

RESULT	ID	Q9QW60	PRELIMINARY;	PRT;	239 AA.
AC	Q9QW60:	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DE	01-MAR-2001 (TREMBLrel. 16, Last annotation update)				
DR	GRB-3-EPIDERMAL GROWTH FACTOR-RECEPTOR-BINDING PROTEIN.				
OS	Mus sp.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxId=10095;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93028373; PubMed=1409582;				
RA	Marcolis B., Silvenoinen O., Comoglio F., Roonprapant C., Skolnik E.,				
RA	Ulrich A., Schlessinger J.;				
RT	"High-efficiency expression/cloning of epidermal growth factor-				
RT	receptor-binding proteins with src homology 2 domains.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 89:8894-8898(1992).				
DR	HSP; Q64010; ICKA.				
DR	Interpro: IPR000980; -				
DR	Interpro: IPR001452; -				
DR	PIfam: PF00017; SH2; 1.				
DR	PIfam: PF00018; SH3; 1.				
DR	PRINTS: PR00401; SH2DOMAIN.				
DR	PRINTS: PR00452; SH3DOMAIN.				
DR	PROSITE: PS50001; SH2; 1.				
DR	PROSITE: PS50002; SH3; 1.				
DR	SMART; SM00326; SH3; 1.				
SQ	SEQUENCE 239 AA; 26013 MW; 483260680C9F09B6 CRC64;				

Query Match 62.2%; Score 1078; DB 11; Length 239;

Best Local Similarity 99.5%; Pred. No. 1.7e-81; Mismatches 1; Indels 0; Gaps 0;

QY	5	AGNFDSEERSWYWGRLSRQEAVALLOGRHGFLVRDSTSPGQYVLVSSENSRVSHYI 64
DB	33	AGNFDSEERSWYWGRLSRQEAVALLOGRHGFLVRDSTSPGQYVLVSSENSRVSHYI 92
QY	65	INSSGRPPVPPSPAPQPPGVSFSLRLIGDQFDSLPALLEFYKIHVDTTLLIEPVARS 124

DB 93 INSSGPRPPVPSAPQPPGSPSRKLGDEPDSLPALLEYKHYHDTTLLEPVARS 152
QY 125 RQSGSVILROEAEYVRALEFNGNDEEDLPFRKGDILIRDRKPEEOMWNAEDSEGRGM 184
DB 153 RQSGSVILROEAEYVRALEFNGNDEEDLPFRKGDILIRDRKPEEOMWNAEDSEGRGM 212
QY 185 IPPYVEKTRPASASVSALIGNOBSS 211
DB 213 IPPYVEKTRPASASVSALIGNOBSS 239

RESULT 2

Q99059 PRELIMINARY; PRT; 255 AA.
AC Q99059;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GAG-CRK PROTEIN (FRAGMENT).
OS Avian sarcoma virus 1.
OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
OX NCBI_Taxid=11957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90045469; PubMed=2554234;
RA Tsuchie H., Chang C.H.W., Yoshida M., Vogt P.K.;
RT "A newly isolated avian sarcoma virus, ASV-L, carries the crk oncogene."
RL Oncogene 4:1281-1284(1989).
CC -1- SIMILARITY: CONTAINS A COPY EACH OF THE SH2 AND SH3 DOMAINS.
DR EMBL: X17292; CA35181.1; -.
DR HSP: 064010; ICKA.
DR InterPro: IPR000980; -.
DR InterPro: IPR001452; -.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR SMART: SM00326; SH3; 1.
KW Oncogene; Polyprotein; SH3 domain; SH2 domain.
FT NON_TER 1 1
FT DOMAIN <1 23 GAG (BY SIMILARITY).
FT DOMAIN 24 253 CRK (BY SIMILARITY).
FT DOMAIN 63 112 SH2 (OR B+C BOX) (BY SIMILARITY).
FT DOMAIN 188 239 SH3 (OR A BOX) (BY SIMILARITY).
FT DOMAIN 254 255 GAG (BY SIMILARITY).
SQ SEQUENCE 255 AA; 27985 MW; 0C562D0B2327A579 CRC64;

Query Match 48.2%; Score 834.5; DB 14; Length 255;
Best Local Similarity 78.3%; Pred. No. 2.5e-61;
Matches 159; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 5 AGFDSSEERSMWGRSLRQEAVALLOGRHGVLEVRDSTSPGDYVLSVSNRSRSHYI 64
DB 52 AGFDSSEERSMWGRSLRQEAVALLOGRHGVLEVRDSTSPGDYVLSVSNRSRSHYI 111
QY 65 INSSGPRPPVPSAPQPPGSPSRKLGDEPDSLPALLEYKHYHDTTLLEPVARS 123
DB 112 VNSLGRAGARRAGGEGRCAPGLNPRFRIRGDEPDSLPALLEYKHYHDTTLLEPVARS 171
QY 124 SROGSGVILROEAEYVRALEFNGNDEEDLPFRKGDILIRDRKPEEOMWNAEDSEGRGM 183
DB 172 SROGSGVILROEAEYVRALEFNGNDEEDLPFRKGDILIRDRKPEEOMWNAEDSEGRGM 231
QY 184 IPPYVEKTRPASASVSALIGNOBSS 206
DB 232 IPPYVEKTRPASASVSALIGNOBSS 254

RESULT 3
Q9NHC3 PRELIMINARY; PRT; 279 AA.
AC Q9NHC3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CELL-CORPSE ENGULFMENT PROTEIN CED-2.
GN CED-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderiinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Reddien P.W., Horvitz H.R.;
RT "CED-2/CrkII and CED-10/Rac control phagocytosis and cell migration in C. elegans."
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL: AF226866; AF33845.1; -.
DR InterPro: IPR000980; -.
DR InterPro: IPR001452; -.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 2.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
SQ SEQUENCE 279 AA; 30878 MW; 5CE7DA478948970B CRC64;

Query Match 19.8%; Score 343; DB 5; Length 279;
Best Local Similarity 31.0%; Pred. No. 1.2e-20;
Matches 93; Conservative 52; Mismatches 111; Indels 44; Gaps 9;

QY 8 FDSSEERSMWGRSLRQEAVALLOGRHGVLEVRDSTSPGDYVLSV---SENSRVS 61
DB 6 FDPFEWRSFYFFPGMSREAHKIL--GEPPVSGTGLMDS--RPEYSLTVREADEGNAYC 63
QY 62 HYIINSGPRPPVPSAPQPPGSPSRKLGDEPDSLPALLEYKHYHDTTLLEPV 121
DB 64 HYLIERGEPR-----EDGTAAGVKTANOSFPDIPALNHFMRVLTASL-- 110
QY 122 ARSROGSGVILROEAEYVRALEFNGNDEEDLPFRKGDILIRDRKPEEOMWNAEDSEGR 181
DB 111 -----AAKKPLIEVVGTFKFTGERETDLPFGGERELILSKINODMWRNALGT 162
QY 182 RGMIPVRYE---KYRPASASVSALIGNOGSHPPQPLGPEPGPYAQPVSNTPLPNLQ- 237
DB 183 TGLVPANYVQIOMERHNDRTS-----KGASQSSIGSGGGAERFSSASTSDNIEL 213
QY 238 --NGPIYARVQKVPANAYDKTALALEVGLYKTKINVSQWGEONCKRGHPRFTHVR 295
DB 214 QRLPEAKAKVTFDRVPNAVYDPTLRVKKGQTVLTQKMSNGMYRAELDQIGSVPHYTLR 273
RESULT 4
Q9PU11 PRELIMINARY; PRT; 217 AA.
AC Q9PU11;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GRB2 PROTEIN.
GN GRB2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Goisset C., Shi D.L., Boucaut J.C.;


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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kung H.-F., Kim J., Huang Y.K., Lin M.C.;
RT "Molecular cloning of two different forms of Xenopus phospholipase C-
gamma-1."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090112; AAD03595.1; -.
DR HSSP; P08487; 2PLD.
DR InterPro; IPR000008; -.
DR InterPro; IPR000909; -.
DR InterPro; IPR000980; -.
DR InterPro; IPR001192; -.
DR InterPro; IPR001452; -.
DR InterPro; IPR001711; -.
DR InterPro; IPR001849; -.
DR InterPro; IPR002048; -.
DR Pfam; PF000017; SH2; 2.
DR Pfam; PF000168; SH3; 1.
DR Pfam; PF00169; C2; 1.
DR Pfam; PF00169; PH; 2.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 2.
DR PROSITE; PS50002; SH3; 1.
DR SMART; SM00239; C2; 1.
FT NON_TER 1 1
FT NON_TER 1067 1067
SQ SEQUENCE 1067 AA; 124019 MW; 533F6876ECDFE5DB CRC64;

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Query Match      11.1%; Score 193; DB 13; Length 1067;
Best local similarity 21.7%; Pred. No. 1.8e-07;
Matches 95; Conservative 43; Mismatches 123; Indels 176; Gaps 17;

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OY 3 GCAGNFDSEER-----SSWYWGRL-----SRQEAVALL-----OGQRHGYFL 39
DB 396 GSOANDDEEOKASNSSELSAEKWFHGKLGAGRDGRHIAERLLTDYCIETGADGGSFL 455
OY 40 VRDSTSPGQYVLSVSENSRVSHYIINS-----SGPR-----KIHYDITLLIEPV 71
DB 456 VRESETFVGDYTLISFWRNKGVQHCRIHSKQEGSPKLLTDNLVESLALITHYQMP 515
OY 72 -----PPVPSPAQ-----PPGVSPSRLR----- 91
DB 516 RCNEFEMRLTEPVQTNHAESKEWYHASLTRQAEHMLKRVPRDGAFLVKKSEQNSYAI 575
OY 92 -----IGDQEFDSLPALEFY-----KIHYDITLLIEPV 121
DB 576 SFRABEKIKHCRVIOEGQSVLSSSEFDSLVDLISYKHPYRKMKLRYPINEETLEKI 635
OY 122 ARSRQSGVILROEAEY-----VRALDFNGNDEEDLPKRGDILIRIRKP 168
DB 636 GTDPDPGALYEGRNPGFVVEANPMPTFKGSYRALFDYKAQREDELTFTKNTIIQNVKQ 695
OY 169 EEDWMAAEDSEGRGM-IVPYVEK-YRPA-----SASVALIG- 206
DB 696 EGGMMWNG-DCGKKQKQWFPANYVEELISPAEPEPERQNLDENSPLGDLGGLVDPSCI 754
OY 207 --NQESRHPQ-----LGGPEPGYAPQSVNTPLNPLONGPIYARVYOKRVPA----- 253
DB 755 ARQDDVHNGRPRFYFTITGLQNLRYPLDVADLLEDMQD---WIKIRKRAQYADARLLEG 811
OY 254 ---YDKTALALEGVELV 267
      : :|||: |||

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DB 812 KIMERKRIALELSELY 828
RESULT 7
OYIHUT 09YHUT PRELIMINARY; PRT; 1010 AA.
ID 09YHUT;
AC 09YHUT;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PHOSPHOLIPASE C-GAMMA-1A (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kung H.-F., Kim J., Huang Y.K., Lin M.C.;
RT "Molecular cloning of two different forms of Xenopus phospholipase C-
gamma-1."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090111; AAD03594.1; -.
DR HSSP; P08487; 2PLD.
DR InterPro; IPR000008; -.
DR InterPro; IPR000909; -.
DR InterPro; IPR000980; -.
DR InterPro; IPR001192; -.
DR InterPro; IPR001452; -.
DR InterPro; IPR001711; -.
DR InterPro; IPR001720; -.
DR InterPro; IPR001849; -.
DR Pfam; PF000017; SH2; 2.
DR Pfam; PF000168; SH3; 1.
DR Pfam; PF00169; C2; 1.
DR Pfam; PF00169; PH; 2.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRINTS; PR00678; PI3KINASEP85.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 2.
DR PROSITE; PS50002; SH3; 1.
DR SMART; SM00252; SH2; 1.
FT NON_TER 1 1
FT NON_TER 1010 1010
SQ SEQUENCE 1010 AA; 116693 MW; 213247F73EE3EEDA CRC64;

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Query Match      10.6%; Score 184.5; DB 13; Length 1010;
Best local similarity 22.5%; Pred. No. 8.5e-07;
Matches 84; Conservative 28; Mismatches 101; Indels 161; Gaps 14;

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OY 3 GCAGNFDSEER-----SSWYWGRL-----SRQEAVALL-----OGQRHGYFL 39
DB 318 GNOANDDEEOKASNSSELSAEKWFHGKLGAGRDGRHIAERLLTDYCIETGADGGSFL 377
OY 40 VRDSTSPGQYVLSVSENSRVSHYIINS-----SGPR-----KIHYDITLLIEPV 71
DB 378 VRESETFVGDYTLISFWRNKGVQHCRIHSKQEGSPKFLITDNLVESLALITHYQMP 437
OY 72 -----PPVPSPAQ-----PPGVSPSRLR----- 91
DB 438 RCNEFEMRLTEPVQTNHAESKEWYHASLTRQAEHMLKRVPRDGAFLVKKSEQNSYAI 497
OY 92 -----IGDQEFDSLPALEFY-----KIHYDITLLIEPV 121
DB 498 SFRABEKIKHCRVIOEGQSVLSSSEFDSLVDLISYKHPYRKMKLRYPINEETLEKI 557
      : :|||: |||

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QY 122 ARSOGSVILROEAEY-----VALFDFNGNDEEDLPFKGDLIRIKRP 168
DB 558 GTPDDYALYEGNPGFYEANPMPTFKCSYALFDYAQRDELTFTKNITIQNEKQ 617
QY 169 EEOWMNAESEGKGM-IPVYVER-YRPASASVALIGNOGESHPOGLGPEPPYRQ 226
DB 618 EGGWNRG-DGGKGRKQMFANMYEILFSP-----PEPPEPQ 653
QY 227 P-SVNTPLPNLQNG 239
DB 654 HLDENSELGLDGG 667

RESULT 8
090279 PRELIMINARY; PRT; 1097 AA.
AC 090279;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE Y116ABC.36 PROTEIN.
GN Y116ABC.36.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabditoidea;
OC Rhabdilitae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RA SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "genome sequence of the nematode C.elegans: A platform for investigating biology";
RT Science 282:2012-2018(1998).
CC -1 SIMILARITY: TO EF-HAND FAMILY.
DR EMBL; AL117204; CAB5138.1; -.
DR HSSP; P29355; ISEM.
DR InterPro; IPR000108; -.
DR InterPro; IPR000194; -.
DR InterPro; IPR000261; -.
DR InterPro; IPR001452; -.
DR InterPro; IPR002046; -.
DR Pfam; PF00018; SH3; 5.
DR Pfam; PF00036; ethand; 2.
DR PRINTS; PRO0499; P67PHOX.
DR PRINTS; PRO0452; SH3DOMAIN.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR PROSITE; PSS0002; SH3; 5.
DR SMART; SM00054; EFh; 1.
DR KEGG; S00054; EFh; 1.
SQ SEQUENCE 1097 AA; 122071 MW; 1C2BA5F103968372 CRC64;

Query Match 10.5%; Score 182; DB 5; Length 1097;
Best Local Similarity 21.2%; Pred. No. 1.5e-06;
Matches 75; Conservative 56; Mismatches 144; Indels 78; Gaps 14;
QY 6 GNDFSESSSYW--WGRLSRQEAVAL-LLOGGRH-----GVFLVRS----- 43
DB 627 GEFDKTASQGFADAFATSNADPFAIAQAPASKGVQSAFNHDTYKCALFAFE 686
QY 44 -STSPDYLVSSENS-----RVSHY-----INSSGPPRPVP 76
DB 687 RSEDELSPEDVITIVOSHAAEPGRAGQLREKVGWFPFAVEAIAAVTPGDPDION 746
QY 77 SPAOPPGVSPSLRIDQDFDSLPALEFYKIHLYDTTLLIPVARSROGSGVILROEE 136
DB 747 MPMPMTSSSSVDQIGVAKARKAEIAA-----MGLTEGGAAPPASNAVAIVISQI 798

QY 137 AEYVALFDFNGNDEEDLPFKGDLIRIKRDPEDQWMAEDSEKGMIPVYVERA 196
DB 799 AQ-----FQWARNNEEDLSPAKGDTIEVLEK-QEMWKGKGNPAGELGWPEKSYVEVGAT 852
QY 197 SASVALIGNOGESHPOGLGPEPPYRQPSV--NTPLPNLQNGP--IYARVIOKRV 250
DB 853 TSTTTPVSPKASA-----GAPGAAGAQDVPSVLTQASFTAPQOOLTYIYDF-- 905
QY 251 PNAVDKTALAEVELYKTKINVGOMEGECNGKRGHPFTHYRLDQOND 303
DB 906 -EAVETDIALHVDGTLIVLEKN-DEWVKGRGNGREGIIPPANYVEISVQAGD 956

RESULT 9
060593 PRELIMINARY; PRT; 640 AA.
AC 060593;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE ARG/ABL-INTERACTING PROTEIN ARGBP2B (FRAGMENT).
GN ARGBP2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RA MEDLINE=97362243; PubMed=9211900;
RA Wang R., Golemis E.A., Krush G.D.;
RT "ArgBP2, a multiple Src homology 3 domain-containing, Arg/Abi-
interacting protein, is phosphorylated in v-Abl-transformed cells and
RT localized in stress fibers and cardiocyte Z-disks";
RT J. Biol. Chem. 272:17542-17550(1997).
RN [2]
RA SEQUENCE FROM N.A.
RA Wang R., Golemis E.A., Krush G.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049885; AAC05509.1; -.
DR HSSP; P29354; IGR1.
DR InterPro; IPR000108; -.
DR InterPro; IPR001452; -.
DR InterPro; IPR002965; -.
DR InterPro; IPR003127; -.
DR Pfam; PF00018; SH3; 2.
DR Pfam; PF02208; Sort; 1.
DR PRINTS; PRO0499; P67PHOX.
DR PRINTS; PRO1217; PRICHEXTENSIN.
DR PRINTS; PRO0452; SH3DOMAIN.
DR PROSITE; PSS0002; SH3; 2.
DR SMART; SM00326; SH3; 1.
DR NON_TER 640 640
SQ SEQUENCE 640 AA; 70660 MW; 030A8C5036331674 CRC64;

Query Match 10.0%; Score 173; DB 4; Length 640;
Best Local Similarity 26.0%; Pred. No. 4.2e-06;
Matches 72; Conservative 29; Mismatches 92; Indels 84; Gaps 12;
QY 43 STSPDYLVSSENSRYSHYINSSGPPRPVPPSPAPQ-----PGVPSRLRIG 93
DB 393 SRTSGRDLGSSSTTLTKSF--TSSSPSSPSRAKDRSPRSTLTLDMGSGAPRERG 450
QY 94 DQEPDSLPALEFKIHLYDTTLLIPVARSROGSGVILROEAEYVALFDFNGNDEED 153
DB 451 TPEKELIPA-----KAVYDKAOTSK 472
QY 154 LFFKKGDLIRIKRDPEDQWMAEDSEKGMIPVYVERAIPVYVERAIPVYVERA 213
DB 473 LSKFGDVTYILRKIDQWYEGE-HGKRVGIFPISYERKLP----- 513
QY 214 QPLGPEPPYRQPSVNTPLPNLQNGPIYARVIOKRVNAYDKTALAEVELYKTKIN 273

Db 770 GQGLFSPSNYE-----ITGPNETANNPP-----AEPQAGP----- 801
QY 240 PIYAVIQRPNVADKTA-----LALEVGLVTKINSGWEGCNGKRGHPPTHV 294
Db 802 -----GKSYKAIYDQAOEDNELSEFEDELIANVDCVDPNMEGCHGRGLFPSNY 854

RESULT 15

O9Y338
ID O9Y338 PRELIMINARY; PRT; 684 AA.
AC O9Y338.
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, last annotation update)
DE SH3P12 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Lin W.S.; Chuang L.M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF136380; AAD27647.1; .
DR HSSP: Q60631; 1GBQ.
DR InterPro: IPR00108; .
DR InterPro: IPR001452; .
DR InterPro: IPR003127; .
DR Pfam: PF00018; SH3; 3.
DR Pfam: PF02208; Sord; 1.
DR PRINTS: PRO0499; P67PROX.
DR PRINTS: PRO0452; SH3DOMAIN.
DR PROSITE: PS50002; SH3; 3.
DR SMART: SM00326; SH3; 1.
SQ SEQUENCE 684 AA; 76341 MW; 2274E632BB07329C CRC64;

Query Match

9.4%; Score 163; DB 4; Length 684;
Best Local Similarity 25.0%; Pred. No. 3e-05;
Matches 67; Conservative 40; Mismatches 103; Indels 58; Gaps 12;

QY 41 RDSSTPGDYVLSVSENSRVSHYINSSGPPRPVPPSPAPOPPGVSPRLRTIGDQFDSL 100
Db 369 RESDAGPGD--LTSLENESQIYKSVLEGVTPLODLSGLKRPSSASATKNSESPRHF--I 424
QY 101 PALLEPYKIHYLDPTTLLIEPVARSROGSGVILROEAEYRALDFNGNDEEDLPFKKD 160
Db 425 PA-----DYLEST---EEFIRRRHD-----DKEMRPARAKFDKQTLKELPLQKGD 468
QY 161 IIRINDKPEEOMWNAEDSGKRGMI PVPYVEKYRPASASVSALIGNQEGSHPOPLGGPE 220
Db 469 IYIYIKQIDQNNYEGE-HHGRVIGIFPRTYIELPPAEK----- 505
QY 221 PGPIYAPSVNTPPLPNQNGPIYARVIQKRVPNAYDKTALALEVGLVTKINSGQW-E 279
Db 506 ---AOPKLTLPVOYLE-----YGEALAKFNFGDTQVEMSEFKGERITLLR-QVDENWYE 556
QY 280 GECNG--KRGHFFTHVRLDQ---QNP 302
Db 557 GRIPGTSROGIFPITYVDYIKRPLVKNP 584

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